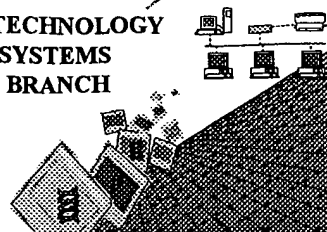


0400

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/042,091
Source: 01PE
Date Processed by STIC: 1/30/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER** **VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/042,091

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ✓ Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/042,091

DATE: 01/30/2002
TIME: 15:27:08

Input Set : A:\ES.txt
Output Set: N:\CRF3\01302002\J042091.raw

pp. 1-3
**Does Not Comply
Corrected Diskette Needed!**

2 <110> APPLICANT: Andrade-Gordon, Patricia
4 Darrow, Andrew
6 Qi, Jensen
W--> 7 <120> TITLE OF INVENTION: DNA Encoding Human Serine Protease EOS
W--> 8 <130> FILE REFERENCE: ORT-1031
W--> 9 <140> CURRENT APPLICATION NUMBER:
C--> 10 <141> CURRENT FILING DATE: 2002-01-08
W--> 11 <160> NUMBER OF SEQ ID: 7
12 <170> SOFTWARE: PatentIn Ver. 2.0

ERRORED SEQUENCES

90 <210> SEQ ID NO: 7
91 <211> LENGTH: 284
92 <212> TYPE: PRT
93 <213> ORGANISM: Homo sapiens
W--> 94 <400> SEQUENCE: 7
95 Met Arg Gly Val Ser Cys Leu Gln Val Leu Leu Leu Val Leu Gly
96 1 5→ 10→ 15→
97 Ala Ala Gly Thr Gln Gly Arg Lys Ser Ala Ala Cys Gly Gln Pro Arg
E--> 98 ~~20~~ 20 25 25 30 30
99 Met Ser Ser Arg Ile Val Gly Gly Arg Asp Gly Arg Asp Gly Glu Trp
E--> 100 35 40 45
101 Pro Trp Gln Ala Ser Ile Gln His Pro Gly Ala His Val Cys Gly Gly
E--> 102 50 55 60
103 Ser Leu Ile Ala Pro Gln Trp Val Leu Thr Ala Ala His Cys Phe Pro
E--> 104 65 70 75 80
105 Arg Arg Ala Leu Pro Ala Glu Tyr Arg Val Arg Leu Gly Ala Leu Arg
E--> 106 85 90 95
107 Leu Gly Ser Thr Ser Pro Arg Thr Leu Ser Val Pro Val Arg Arg Val
E--> 108 100 105 110
109 Leu Leu Pro Pro Asp Tyr Ser Glu Asp Gly Ala Arg Gly Asp Leu Ala
E--> 110 115 120 125
111 Leu Leu Gln Leu Arg Arg Pro Val Pro Leu Ser Ala Arg Val Gln Pro
E--> 112 130 135 140
113 Val Cys Leu Pro Val Pro Gly Ala Arg Pro Pro Pro Gly Thr Pro Cys
E--> 114 145 150 155 160
115 Arg Val Thr Gly Trp Gly Ser Leu Arg Pro Gly Val Pro Leu Pro Glu
E--> 116 165 170 175
117 Trp Arg Pro Leu Gln Gly Val Arg Val Pro Leu Leu Asp Ser Arg Thr
E--> 118 180 185 190
119 Cys Asp Gly Leu Tyr His Val Gly Ala Asp Val Pro Gln Ala Glu Arg

see p. 2
*misaligned
amino acid
numbers.
(see item 3
on Error
Summary Sheet)*

DATE: 01/30/2002

TIME: 15:27:09

Output Set: N:\CRF3\01302002\J042091.raw

```

E--> 120 195                200                205
      121 Ile Val Leu Pro Gly Ser Leu Cys Ala Gly Tyr Pro Gln Gly His Lys
E--> 122 210                215                220
      123 Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Thr Cys Leu Gln Ser
E--> 124 225                230                235                240
      125 Gly Ser Trp Val Leu Val Gly Val Val Ser Trp Gly Lys Gly Cys Ala
E--> 126 245                250                255
      127 Leu Pro Asn Arg Pro Gly Val Tyr Thr Ser Val Ala Thr Tyr Ser Pro
E--> 128 260                265                270
      129 Trp Ile Gln Ala Arg Val Thr Ser Asn Ala Ser Arg
E--> 130 275                280
E--> 131 - 6 -
      135 ORT-1031

```

same
env

all next page for more error

<210> 2
<211> 20
<212> DNA
<213> Artificial Sequence
<220>

<223> Description of Artificial Sequence:

oligonucleotide

<400> 2

gagaaagtca gattcacagc

<210> 3

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

oligonucleotide

insufficient explanation - give source of genetic material

20

(see item 11 on Eval Summary Sheet)

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/042,091

DATE: 01/30/2002

TIME: 15:27:10

Input Set : A:\ES.txt

Output Set: N:\CRF3\01302002\J042091.raw

L:7 M:283 W: Missing Blank Line separator, <120> field identifier
L:8 M:283 W: Missing Blank Line separator, <130> field identifier
L:9 M:283 W: Missing Blank Line separator, <140> field identifier
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:11 M:283 W: Missing Blank Line separator, <160> field identifier
L:13 M:283 W: Missing Blank Line separator, <210> field identifier
L:17 M:283 W: Missing Blank Line separator, <400> field identifier
L:49 M:283 W: Missing Blank Line separator, <220> field identifier
L:52 M:283 W: Missing Blank Line separator, <400> field identifier
L:58 M:283 W: Missing Blank Line separator, <220> field identifier
L:61 M:283 W: Missing Blank Line separator, <400> field identifier
L:67 M:283 W: Missing Blank Line separator, <220> field identifier
L:70 M:283 W: Missing Blank Line separator, <400> field identifier
L:76 M:283 W: Missing Blank Line separator, <220> field identifier
L:79 M:283 W: Missing Blank Line separator, <400> field identifier
L:85 M:283 W: Missing Blank Line separator, <220> field identifier
L:88 M:283 W: Missing Blank Line separator, <400> field identifier
L:94 M:283 W: Missing Blank Line separator, <400> field identifier
L:98 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7
M:332 Repeated in SeqNo=7